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[About EBI](#)
[Research](#)
[Services](#)
[Toolbox](#)
[Databases](#)
[Downloads](#)

SEQUENCE ANALYSIS

- [Help Index](#)
- [General Help](#)
- [Formats](#)
- [Gaps](#)
- [Matrix](#)
- [References](#)
- [Clustalw Help](#)

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CLUSTAL W (1.82) Multiple Sequence Alignments

```

Sequence format is Pearson
Sequence 1: FixL          505 aa
Sequence 2: SEQ76        153 aa
Start of Pairwise alignments
Aligning...
Sequences (1:2) Aligned. Score: 17
Guide tree      file created: [/ebi/extserv/old-work/clust
Start of Multiple Alignment
There are 1 groups
Aligning...
Group 1:                               Delayed
Sequence:2      Score:1222
Alignment Score 83
CLUSTAL-Alignment file created [/ebi/extserv/old-work/clustal

```

clustalw-20030805-21191830.aln

CLUSTAL W (1.82) multiple sequence alignment

```

FixL      MAPTRVTHPPDDGRGEHFRVRIEGFGVGTWDLDLKTWALDWSDTAI
SEQ76     -----VLSEGEWQLVLHVWAKVEADVA-
              .. * *: * *: * *: * *: * *: *
FixL      LFLSRLEPDDRERVESAIKRVSERGGGFDVSFRVAGTSNAGQWIR/

```

```
SEQ76 -----
FixL
SEQ76 LSGIFLDIDEEKQVEGALRTRETHLRSILHTIPDAMIVIDGHGIIQ
-----ILII
:::
FixL
SEQ76 LEAIGQNVNILMPEPDRSRHDSYISRYRTTSDPHIIGIGRIVTGKI
FKHLKTEAEMKASEDLKKHGVTVLT-----ALGAILKKK-
::: : : : : * : : : : : : : : * * : *
FixL
SEQ76 MQSGGEPYFTGFVRDLTEHQQTQARLQELQSELVHVSRLSAMGEM
HEAELKPLAQ---SHATKHKIPIKYLEFISEAIIHVLHSRHPGDFC
:: : * : * : : * : : : * : * : :
FixL
SEQ76 SNYMKGSRRLLAGSSDPNTPKVESALDRAAEQALRAGQIIRRLRDI
RKDIAAKYKELGYQG-----
: : : : * :
FixL
SEQ76 KLIEEAGALGLAGAREQNVQLRFSLDPGADLVLADRVQIQQVLVNI
-----
FixL
SEQ76 ELVVTNTPAADDMIEVEVSDTGSGFQDDVIPNLFQTFFTTKDTGMC
-----
FixL
SEQ76 GRMWAESNASGGATFRFTLPAADEN 505
-----
```

clustalw-20030805-21191830.dnd

(FixL:0.41176,SEQ76:0.41176);

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Protein

Genome

Structure

PMC

Taxonomy

OMIM

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Clipboard

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Get Subsequence

1: P23222. Sensor protein fixL...[gi:120207]

BLink, Domains, Links

LOCUS P23222 505 aa linear BCT 15-SEP-2003
 DEFINITION Sensor protein fixL.
 ACCESSION P23222
 VERSION P23222 GI:120207
 DBSOURCE swissprot: locus FIXL_BRAJA, accession P23222;
 class: standard.
 created: Nov 1, 1991.
 sequence updated: Nov 1, 1991.
 annotation updated: Sep 15, 2003.
 xrefs: gi: 39522, gi: 39523, gi: 3021308, gi: 3021311, gi:
 27350985, gi: 27351017, gi: 7465577, pdb accession 1DRM, pdb
 accession 1LT0, pdb accession 1DP6, pdb accession 1DP8, pdb
 accession 1DP9, pdb accession 1LSV, pdb accession 1LSW, pdb
 accession 1LSX
 xrefs (non-sequence databases): InterProIPR003594,
 InterProIPR004358, InterProIPR003661, InterProIPR005467,
 InterProIPR001610, InterProIPR000700, InterProIPR000014,
 PfamPF02518, PfamPF00512, PfamPF00785, PfamPF00989, PRINTSPR00344,
 SMARTSM00387, SMARTSM00388, SMARTSM00086, SMARTSM00091,
 TIGRFAMsTIGR00229, PROSITEPS50109, PROSITEPS50113, PROSITEPS50112
 KEYWORDS Sensory transduction; Transferase; Kinase; Phosphorylation; Heme;
 Transmembrane; Inner membrane; Nitrogen fixation; Repeat; Iron
 transport; 3D-structure; Complete proteome.
 SOURCE Bradyrhizobium japonicum
 ORGANISM Bradyrhizobium japonicum
 Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 Bradyrhizobiaceae; Bradyrhizobium.
 REFERENCE 1 (residues 1 to 505)
 AUTHORS Anthamatten,D. and Hennecke,H.
 TITLE The regulatory status of the fixL- and fixJ-like genes in
 Bradyrhizobium japonicum may be different from that in Rhizobium
 meliloti
 JOURNAL Mol. Gen. Genet. 225 (1), 38-48 (1991)
 MEDLINE 91155933
 PUBMED 2000090
 REMARK SEQUENCE FROM N.A.
 STRAIN=USDA 110spc4
 REFERENCE 2 (residues 1 to 505)
 AUTHORS Kaneko,T., Nakamura,Y., Sato,S., Minamisawa,K., Uchiyama,T.,
 Sasamoto,S., Watanabe,A., Idesawa,K., Iriguchi,M., Kawashima,K.,
 Kohara,M., Matsumoto,M., Shimpo,S., Tsuruoka,H., Wada,T., Yamada,M.
 and Tabata,S.
 TITLE Complete genomic sequence of nitrogen-fixing symbiotic bacterium
 Bradyrhizobium japonicum USDA110
 JOURNAL DNA Res. 9 (6), 189-197 (2002)
 MEDLINE 22484998
 PUBMED 12597275

REMARK SEQUENCE FROM N.A.
STRAIN=USDA 110

REFERENCE 3 (residues 1 to 505)

AUTHORS Gong,W., Hao,B., Mansy,S.S., Gonzalez,G., Gilles-Gonzalez,M.A. and Chan,M.K.

TITLE Structure of a biological oxygen sensor: a new mechanism for heme-driven signal transduction

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 95 (26), 15177-15182 (1998)

MEDLINE 99079986

PUBMED 9860942

REMARK X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 154-270.

REFERENCE 4 (residues 1 to 505)

AUTHORS Gong,W., Hao,B. and Chan,M.K.

TITLE New mechanistic insights from structural studies of the oxygen-sensing domain of Bradyrhizobium japonicum FixL

JOURNAL Biochemistry 39 (14), 3955-3962 (2000)

MEDLINE 20213243

PUBMED 10747783

REMARK X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 154-270.

COMMENT

This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. The original entry is available from <http://www.expasy.ch/sprot> and <http://www.ebi.ac.uk/sprot>

[FUNCTION] PUTATIVE OXYGEN SENSOR; MODULATES THE ACTIVITY OF FIXJ, A TRANSCRIPTIONAL ACTIVATOR OF NITROGEN FIXATION FIXK GENE. FIXL PROBABLY ACTS AS A KINASE THAT PHOSPHORYLATES FIXJ.

[ENZYME REGULATION] HEMOPROTEIN. THE HEME MOIETY REGULATES THE KINASE ACTIVITY.

[SUBCELLULAR LOCATION] Integral membrane protein. Inner membrane.

[SIMILARITY] Contains 1 histidine kinase domain.

[SIMILARITY] Contains 2 PAS (PER-ARNT-SIM) dimerization domains.

[SIMILARITY] Contains 2 PAS-associated C-terminal (PAC) domains.

FEATURES	Location/Qualifiers
source	1..505 /organism="Bradyrhizobium japonicum" /db_xref="taxon:375"
gene	1..505 /gene="FIXL" /note="synonym: BLL2760"
Protein	1..505 /gene="FIXL" /product="Sensor protein fixL" /EC_number="2.7.3.-"
Region	14..85 /gene="FIXL" /region_name="Domain" /note="PAS 1."
Region	88..140 /gene="FIXL" /region_name="Domain" /note="PAC 1."
Region	141..208 /gene="FIXL" /region_name="Domain" /note="PAS 2."
Region	155..160 /gene="FIXL"

<u>Region</u>	/region_name="Beta-strand region" 161..162 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 164..168 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 170..176 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 180..183 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 184..185 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 187 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 188..191 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 194..195 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 196..210 /gene="FIXL"
<u>Site</u>	/region_name="Helical region" 200 /gene="FIXL"
	/site_type="metal-binding"
<u>Region</u>	/note="IRON (HEME AXIAL LIGAND)." 209..268 /gene="FIXL"
<u>Region</u>	/region_name="Domain" /note="PAC 2." 216..218 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 220..225 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 227..228 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 231..243 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 244..245 /gene="FIXL"
<u>Region</u>	/region_name="Hydrogen bonded turn" 246..255 /gene="FIXL"
<u>Region</u>	/region_name="Beta-strand region" 257..268 /gene="FIXL"
<u>Region</u>	/region_name="Helical region" 269 /gene="FIXL"
	/region_name="Hydrogen bonded turn"

Region 288..503
/gene="FIXL"
/region_name="Domain"
/note="HISTIDINE KINASE."
Site 291
/gene="FIXL"
/site_type="phosphorylation"
/note="(AUTO-) (BY SIMILARITY)."

ORIGIN

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61 lfslrlepdd rervesaikr vserrgggfdv sfrvagtsna gqwiraragl irdeagtarh
121 lsgifldide ekqvegalrt rethlrsilh tipdamivid ghgiiqlfst aaerlfgwse
181 leaigqnvni lmpepdrsrh dsyisryrtt sdphiigigr ivtgkrrdgt tfpmhlsige
241 mqsggpepyft gfvrldtehq qtqarlqelq selvhvsrls amgemasala helnqplaa
301 snymkgsrrl lagssdpntp kvesaldras eqalragqii rrlrdfvarg esekrvesls
361 klieeagalg lagareqnvq lrfsldpgad lvladrvgiq qvlvnlfrna leamaqsqrr
421 elvvtntpaa ddmieevsd tgsgfqddvi pnlftqfttt kdtgmvgvls isrsiieahg
481 grmwaesnas ggatfrftlp aaden
```

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Jul 30 2003 12:44:50